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Docket No: 10806-152

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 to Mail Stop Fee Amendment; Commissioner for Patents; P.O. Box
 1450; Alexandria, VA at facsimile number 703-308-0294 on
 October 14, 2003.

Raymond J. Anderson

IN THE UNITED STATES PATENT & TRADEMARK OFFICE

Applicant: Anneli Attersand : Paper No.
 Serial No.: 09/990,415 : Group Art Unit: 1653
 Filing Date: November 21, 2001 : Examiner: C.M. Kam
 For: Gene Encoding Protein Cluster I and the Encoded Protein

RESPONSE

Mail Stop Fee Amendment
 Commissioner for Patents
 P.O. Box 1450
 Alexandria, VA 22313-1450

Dear Sir:

In the Official Action dated July 31, 2003, the Examiner required restriction under 35 U.S.C. §121 between claims 1, 4-7 and 9 drawn to nucleic acids, vectors, host cells and methods for producing polypeptides, claims 2 and 3 drawn to polypeptides encoded by nucleic acid, and claim 8 drawn to a method for identifying an agent capable of modulating a nucleic acid. Applicant hereby elects the invention of claims 1, 4-7 and 9. This election is made with traverse on the basis that it would not be unduly burdensome for the Examiner to examine all of the claims in this application.

The Examiner further indicated in the Official Action that should group I, claims 1, 4-7 and 9, b elected, Applicant is required to select one nucleotide sequence identified by SEQ ID NO from claim 1 as any nucleic acid is considered, absent factual data to the contrary, a distinct nucleotide. The Examiner specifically noted this is not a species election.

Applicant hereby elects SEQ ID NO: 1, with traverse. Traversal is made on the basis that it

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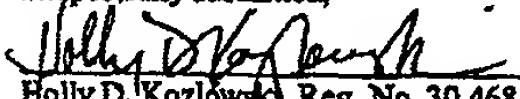
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would not be unduly burdensome for the Examiner to examine all of sequences 1, 3, 5 and 7 as recited in claims 1, 4-7 and 9. As set forth in the specification, for example, in the technical field, the invention relates to the identification of a human gene family expressed in metabolically relevant tissues, which genes encode a group of polypeptides referred to as 'protein cluster I'. In example 2 of the present application, analysis of protein cluster I, the alignment analysis shows a high degree of conservation in two separate regions, indicating a presence of two novel domains. In view of the homology, Applicant submits that it would not be unduly burdensome for the Examiner to examine all of SEQ ID NOS: 1, 3, 5 and 7 in this application. Reconsideration of this portion of the restriction requirement is therefore respectfully requested.

Examination on the merits is requested.

Respectfully submitted,


Holly D. Kozlowski, Reg. No. 30,468
DINSMORE & SHOHL LLP
1900 Chemed Center
255 East Fifth Street
Cincinnati, Ohio 45202
(513) 977-8568

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